

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:45:24 ; Search time 3.52121 Seconds

(without alignments)
977.656 Million cell updates/sec

Title: US-09-988-971-2_COPY_94_176

Sequence: 1 WLVEGHSREKAEKELLPGN.....WLVSPLTFPLQALVDHY 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	254	57.0	504	1	HCK_MACFA
2	254	57.0	504	1	HCK_HUMAN
3	242	54.3	511	1	LYN_HUMAN
4	241	54.0	503	1	HCK_RAT
5	241	54.0	511	1	LYN_MOUSE
6	241	54.0	511	1	LYN_RAT
7	240	53.8	524	1	HCK_MOUSE
8	233.5	52.1	504	1	HCK_HUMAN
9	228	51.1	508	1	LCK_HUMAN
10	227	50.9	508	1	LCK_MOUSE
11	224.5	50.3	498	1	BLK_MOUSE
12	223	50.0	507	1	LCK_CHICK
13	217	48.7	544	1	YES_XIPHE
14	215	48.2	537	1	YES_XENLA
15	214	48.0	541	1	YES_CHICK
16	212	47.5	529	1	FGF_HUMAN
17	212	47.5	543	1	YES_HUMAN
18	211	47.3	541	1	YES_MOUSE
19	210	47.1	517	1	FGF_MOUSE
20	209	46.9	533	1	LYN_MOUSE
21	207	46.4	528	1	YES_AVISY
22	207	46.4	545	1	FGF_FSVGR
23	206	46.2	533	1	FGF_CHICK
24	206	46.2	536	1	FGF_HUMAN
25	205	46.0	539	1	YES_CANPA
26	203	45.5	536	1	FGF_XENLA
27	197	44.2	536	1	LYN_XIPHE
28	195	43.7	535	1	YRK_CHICK
29	187	41.9	552	1	SRC1_DROME
30	186	41.7	526	1	SRC_AVISR
31	186	41.7	526	1	SRC_RSVSR
32	186	41.7	532	1	SRC_CHICK
33	186	41.7	557	1	SRC_AVISR

34	186	41.7	587	1	SRC_AVIS2
35	185	41.5	568	1	SRC_AVIS5
36	184.5	41.4	506	1	SRC4_SPOA
37	179	40.1	523	1	SRC_RSPA
38	177	39.7	526	1	SRC_RSPV
39	177	39.7	535	1	SRC_HUMAN
40	177	39.7	535	1	SRC_RAT
41	177	39.7	540	1	SRC_MOUSE
42	176.5	39.6	496	1	SRM_MOUSE
43	173	38.8	531	1	SRC2_XENLA
44	172	38.6	526	1	SRC_RSVH1
45	171.5	38.5	509	1	STK_HYDAT

ALIGNMENTS

RESULT 1	HCK_MACFA	STANDARD	PRT	504 AA.	PL15054 avian sarco
ID	HCK_MACFA				P14084 avian sarco
AC	Q95M30				P42699 spongilla 1
DT	15-JUN-2002 (Rel. 41, Created)				P31693 rous sarcom
DT	15-JUN-2002 (Rel. 41, Last sequence update)				P00526 rous sarcom
DT	15-JUN-2002 (Rel. 41, Last annotation update)				P12931 homo sapien
DE	Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell kinase).				Q9w4d9 rattus norv
GN	HCK.				P05480 mus musculu
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).				O62270 mus musculu
OC	Bucaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				P1316 xenopus lae
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;				P25020 rous sarcom
OC	Cercopithecoidea; Macaca.				P17713 hydra atten
OX	NCBI_Taxid=9541;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Picard C.;				
RL	Thesis (2001), University of Marseille, France.				
CC	- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC				
CC	RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO				
CC	CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE				
CC	DEGRADATION PROCESS OF NEUTROPHILS (By similarity).				
CC	- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein				
CC	tyrosine phosphate.				
CC	- SUBCELLULAR LOCATION: Membrane-associated (By similarity).				
CC	- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC				
CC	SUBFAMILY.				
CC	- SIMILARITY: CONTAINS 1 SH2 DOMAIN.				
CC	- SIMILARITY: CONTAINS 1 SH3 DOMAIN.				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: AJ320181; CAC44031.1; -				
DR	InterPro: IPR0000719; Euk_Pkinase.				
DR	InterPro: IPR000980; SH2.				
DR	InterPro: IPR001452; SH3.				
DR	InterPro: IPR001245; Tyr_kinase.				
DR	Pfam: PF00017; SH2; 1.				
DR	Pfam: PF00018; SH3; 1.				
DR	Pfam: PF00069; pkinase; 1.				
DR	ProDom: PD000001; Euk_Pkinase; 1.				
DR	ProDom: PD000066; SH3; 1.				
DR	ProDom: PD000093; SH2; 1.				
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.				
DR	PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.				
DR	PROSITE: PS00001; SH2; 1.				
DR	PROSITE: PS00002; SH3; 1.				
KW	Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;				

KM Myristate; SH2 domain; SH3 domain.
 FT DOMAIN 56 116
 FT DOMAIN 122 219 SH3.
 FT DOMAIN 240 493 PROTEIN KINASE.
 FT NP BIND 246 254 ATP (BY SIMILARITY).
 FT BINDING 268 268 ATP (BY SIMILARITY).
 FT ACT SITE 359 359 BY SIMILARITY.
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT MOD_RES 389 389 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 504 AA; 57096 MW; 5382932202DE3423 CRC64;
 Query Match 57.0%; Score 254; DB 1; Length 504;
 Best Local Similarity 57.8%; Pred. No. 1.7e-22;
 Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
 Qy 1 WLYEGLSREKAEELLPLPGNGCAFILRSQTRRSYSLSVRLSPASMDRIRHRLHCL 60
 Db 122 WFFGIGSRKDAERQLLAPGNMLGSFMRISSETTKSYSLSVRYDPRQGVKHKIRTL 181
 Qy 61 DNGWLYISPRITFPLQLALVDHY 83
 Db 182 DNGGFYISPRSTFSTLQELVDHY 204
 RESULT 2
 HCK_HUMAN STANDARD; PRT; 526 AA.
 AC P08631; Q96CC0; Q9H5Y5; Q9NUA4; Q9UMJ5;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (559-HCK and P60-HCK)
 DE (hemopoietic cell kinase).
 GN HCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE OF 22-526 FROM N.A.
 RX MEDLINE=87257942; PubMed=3496523;
 RA Quintrell N., Ledo R., Varmus H., Bishop J.M., Pettenati M.J.,
 RA le Beau M.M., Diaz M.O., Rowley J.D.;
 RT "Identification of a human gene (HCK) that encodes a protein-tyrosine
 RT kinase and is expressed in hemopoietic cells.";
 RL Mol. Cell. Biol. 7:2267-2275(1987).
 RN [2]
 RP SEQUENCE OF 22-526 FROM N.A.
 RX MEDLINE=87257943; PubMed=3453117;
 RA Ziegler S.F., March J.D., Lewis D.B., Perlmutter R.M.;
 RT "Novel protein-tyrosine kinase gene (hck) preferentially expressed in
 RT cells of hematopoietic origin.";
 RL Mol. Cell. Biol. 7:2276-2285(1987).
 RN [3]
 RP SEQUENCE OF 22-526 FROM N.A.
 RX TISSUE-B-cell;
 RA Strausberg R.;
 RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 22-526 FROM N.A.
 RC TISSUE=ileal mucosa;
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakejima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Oca T., Suzuki Y.,
 RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 RA Isega T., Sugano S.;
 RT "NED0 human cDNA sequencing project.";
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloakas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Beggsley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark S.Y., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Frazer A., French L., Garner P.,
 RA Gratlam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hamble D., Harley J.L., Heath P.D., Ho S., Holden K., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levasailho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMuray A.A.,
 RA Milne S.K., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.U.C.T., Pratchall S.R., Plumb R.W., Ramsey H.,
 RA Rice C.M., Ross W.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilmings L., Wray P.W., Hubbard T., Dublin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [6]
 RP SEQUENCE OF 179-526 FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=92241680; PubMed=1572549;
 RA Haderitzky D., Strehardt K., Ruesamen-Waigmann H.;
 RT "The genomic locus of the human hemopoietic-specific cell protein
 RT tyrosine kinase (PTK) encoding gene (HCK) contains conservation of
 RT exon-intron structure among human PTKs of the scr family.";
 RL Gene 113:275-280(1992).
 RN [7]
 RP SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
 RX MEDLINE=91342636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsey R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization.";
 RL Mol. Cell. Biol. 11:4363-4370(1991).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 78-526.
 RX MEDLINE=97177106; PubMed=9024658;
 RA Slicheri F., Moarefi I., Kurivan J.;
 RT "Crystal structure of the Src family tyrosine kinase Hck.";
 RL Nature 385:602-609(1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 81-137.
 RX MEDLINE=98453315; PubMed=9778343;
 RA Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,
 RA Labbury J.E.;
 RT "RT loop flexibility enhances the specificity of Src family SH3
 RT domains for HIV-1 Nef.";
 RL Biochemistry 37:14683-14691(1998).
 RN [10]
 RP STRUCTURE BY NMR OF 78-138.
 RX MEDLINE=98239731; PubMed=9571048;
 RA Horita D.A., Baldissari D.M., Zhang W., Altieri A.S., Smithgall T.E.,
 RA Gmeiner W.H., Byrd R.A.;
 RT "Solution structure of the human Hck SH3 domain and identification of
 RT its ligand binding site.";
 RL J. Mol. Biol. 278:253-265(1998).
 RN [11]
 RP STRUCTURE BY NMR OF 139-245.
 RX MEDLINE=97263487; PubMed=9109402;
 RA Zhang W., Smithgall T.E., Gmeiner W.H.;
 RT "Sequential assignment and secondary structure determination for the
 RT Src homology 2 domain of hematopoietic cellular kinase.";
 RL FEBS Lett 406:131-135(1997).
 CC - FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO

CC CONTRIBUTOR TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: P60-HCK AND P59-HCK ARE ASSOCIATED WITH
 CC MEMBRANES. P60-HCK IS ALSO CYTOPLASMIC (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; P60-HCK (shown here) and P59-
 CC HCK; are produced by alternative initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 CC MYELOID AND B-LYMPHOID LINEAGES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 DR EMBL; M16591; AAA52643.1; -;
 DR EMBL; M16592; AAA52644.1; -;
 DR EMBL; BC014435; AAH14435.1; -;
 DR EMBL; AK026432; BAB15482.1; -;
 DR EMBL; AL049539; CAB75606.1; -;
 DR EMBL; X58741; CAA1565.2; -;
 DR EMBL; X58742; CAA1565.2; JOINED.
 DR EMBL; X58743; CAA1565.2; JOINED.
 DR PIR; A27812; TVHUC.
 DR PDB; 2HCK; 20-AUG-97.
 DR PDB; 3HCK; 15-OCT-97.
 DR PDB; 4HCK; 17-JUN-98.
 DR PDB; 5HCK; 17-JUN-98.
 DR PDB; 1AD5; 15-MAY-97.
 DR PDB; 1BU1; 11-NOV-98.
 DR Genew; HGNC:4840; HCK.
 DR MIM; 142370; -;
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00069; pkinase; 4.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00352; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR K1; Tyrosinase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 DR K1; Tyrosinase; SH2 domain; SH3 domain; Alternative initiation;
 DR K1; 3D-structure.
 FT CHAIN 1 526 TYROSINE-PROTEIN KINASE P60-HCK.
 FT INIT MET 22 526 TYROSINE-PROTEIN KINASE P59-HCK.
 FT DOMAIN 78 138 FOR ISOFORM P59-HCK.
 FT DOMAIN 144 241 SH2.
 FT DOMAIN 262 315 PROTEIN KINASE.
 FT NP_BIND 268 276 ATP.
 FT BINDING 290 290 ATP.
 FT ACT SITE 381 381 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT LIPID 23 23 MYRISTATE (BY SIMILARITY).

FT MOD RES 411 411 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 24 24 C -> S (IN REF. 1).
 FT CONFLICT 144 144 W -> R (IN REF. 4).
 FT SEQUENCE 526 AA; 53599 MW; 847817A0A41725 CRC64;
 SQ
 Query Match 57.0%; Score 254; DB 1; Length 526;
 Best Local Similarity 57.8%; Pred. No. 1.8e-22;
 Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
 QY 1 MLYSGSRKAEELLPGNGAFIPRESQSGSYSLSRSPASMDRIHRHICL 60
 DB 144 WFFGKSRKDAERQLAPGNLGSFMRISRTTKSGTSLSVRDYDPROGQVKAHKTITL 203
 QY 61 DNGEWYISPLTLPSPALVDHY 83
 DB 204 DNGGFYISPRSTFSTLQELVDHY 226
 RESULT 3
 LYN HUMAN
 ID LYN HUMAN STANDARD; PRT; 511 AA.
 AC P07948;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=87127210; PubMed=3561390;
 RA Yananashi Y., Fukushima S.-I., Semba K., Sukeyama J., Miyajima N.,
 RA Matsubara K.-I., Yamamoto T., Toyoshima K.;
 RT "The yes-related cellular gene lyn encodes a possible tyrosine kinase
 RT similar to p56lck.";
 RL Mol. Cell. Biol. 7:237-243(1987).
 RN [2]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=94171041; PubMed=8125304;
 RA Rieger L.G., Raben N., Miller L., Jelsema C.;
 RT "The CDNs encoding two forms of the lyn protein tyrosine kinase are
 RT expressed in rat mast cells and human myeloid cells.";
 RL Gene 138:219-222(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL; M16038; AAA59540.1; -;
 DR EMBL; M79321; AAB50019.1; -;
 DR PIR; A26719; TVHULY.
 DR HSSP; P08631; 1AD5.
 DR Genew; HGNC:6735; LYN.
 DR MIM; 165120; -;
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0 BY SIMILARITY.
 FT LIPID 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH3.
 FT DOMAIN 128 225 SH2.
 FT DOMAIN 246 500 PROTEIN KINASE.
 FT NP BIND 252 260 ATP (BY SIMILARITY).
 FT BINDING 274 274 ATP (BY SIMILARITY).
 FT ACT SITE 366 366 BY SIMILARITY.
 FT MOD RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).
 FT VARSPIC 42 MISSING (IN ISOPORN LYN B).
 FT SEQUENCE 511 AA; 58442 MW; 8419CD461204E364 CRC64;

Query Match 54.3%; Score 242; DB 1; Length 511;
 Best Local Similarity 54.2%; Pred. No. 4,6e-21;
 Matches 45; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 1 WLYEGLSRKAEELLRLPGNPGAFLLRESQTRRGYSLSVRLSPASMDRIHRYHCL 60
 DB 128 WFKDITRKDAERQLAPGNMGLSFMIRDETTKGSYSVRLDPDPOHGVTVHYKIRTL 187

QY 61 DNGMWYISPRITPSPQLAVDHY 83
 DB 188 DNGGYISPRITPSPQLAVDHY 210

RESULT 4
 HCK_RAT STANDARD; PRT; 503 AA.

AC P50545; Q64647;
 DC 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell
 kinase).
 GN HCK.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92109719; PubMed=1764064;
 RX Okano Y., Sugimoto Y., Fukuoaka M., Matsui A., Nagata K.I., Nozawa Y.,
 RT "Identification of rat cDNA encoding hck tyrosine kinase from
 megakaryocytes";
 RL Biochem. Biophys. Res. Commun. 181:1137-1144(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WiStar; TISSUE=Spleen;
 RA Vajjala Gouri B.S., Renu V., Kanakar S., Swarn G.;
 RT "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and
 characterization of its gene product.";

RL J. BioSci. 19:117-123(1994).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: S74141; AAB20754.1; -
 CC EMBL: M63666; AAA41312.1; -
 CC EMBL: X62345; CAA44218.1; -
 CC HSSP: P08631; 1B01.
 CC InterPro: IPR000719; Euk_pkinase.
 CC InterPro: IPR000980; SH2.
 CC InterPro: IPR001245; Tyr_pkinase.
 CC InterPro: IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain.
 FT MYRISTATE; SH2 domain; SH3 domain.
 FT DOMAIN 55 115 SH3.
 FT DOMAIN 121 218 SH2.
 FT DOMAIN 239 492 PROTEIN KINASE.
 FT NP BIND 245 253 ATP (BY SIMILARITY).
 FT BINDING 267 267 ATP (BY SIMILARITY).
 FT ACT SITE 358 358 BY SIMILARITY.
 FT LIPID 2 MYRISTATE (BY SIMILARITY).
 FT MOD_RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 51 51 F -> V (IN REF. 2).
 FT CONFLICT 205 205 K -> R (IN REF. 2).
 FT CONFLICT 306 306 I -> T (IN REF. 2).
 FT SEQUENCE 503 AA; 57016 MW; A1FC1F3F082P73 CRC64;

Query Match 54.0%; Score 241; DB 1; Length 503;
 Best Local Similarity 56.6%; Pred. No. 5,9e-21;
 Matches 47; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 1 WLYEGLSRKAEELLRLPGNPGAFLLRESQTRRGYSLSVRLSPASMDRIHRYHCL 60
 DB 121 WFKDITRKDAERQLAPGNMGLSFMIRDETTKGSYSVRLDPDPOHGVTVHYKIRTL 180

QY 61 DNGMWYISPRITPSPQLAVDHY 83
 DB 181 DSGGYISPRITPSPQLAVDHY 203

RESULT 5
LYN_MOUSE
ID LYN_MOUSE STRAND: PRT; 511 AA.
AC P25911; Q62127;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
GN LYN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91260688; PubMed=1710766;
RA Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A.,
RA Lock P., Dunn A.R.;
RT "Alternatively spliced murine lyn mRNAs encode distinct proteins";
RL Mol. Cell. Biol. 11:3399-3406(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91203857; PubMed=2017160;
RA Yi T., Bolen J.B., Ihle J.N.;
RT "Hematopoietic cells express two forms of lyn kinase differing by 21
RT amino acids in the amino terminus";
RL Mol. Cell. Biol. 11:2391-2396(1991).
RN [3]
RP SEQUENCE OF 363-431 FROM N.A.
RX MEDLINE=90152381; PubMed=2482828;
RA Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;
RT "The application of the polymerase chain reaction to cloning members
RT of the protein tyrosine kinase family";
RL Gene 85:67-74(1989).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
CC MYELOID CELLS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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DR EMBL; M64608; AAA39470.1; -
DR EMBL; M57696; AAA39471.1; -
DR EMBL; M57697; AAA39472.1; -
DR EMBL; M33426; AAA40017.1; -
DR PIR; A39719; A39719.
DR HSSP; P08631; IAD5.
DR MGJ; MGJ:96892; LYN.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PRO0452; SH3DOMAIN.
DR PRINTS; PRO0109; TYRKINASE.
DR ProDom; PD000001; Euk_Pkinase; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00219; TYK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
KW Palmitate; Lipoprotein; Alternative splicing.
FT INTR. MET 0
FT LIPID 1
FT LIPID 2
FT DOMAIN 62
FT DOMAIN 122
FT DOMAIN 128
FT DOMAIN 225
FT DOMAIN 246
FT NP_BIND 252
FT BINDING 260
FT BINDING 274
FT ACT_SITE 274
FT ACT_SITE 366
FT MOD_RES 366
FT MOD_RES 396
FT VAR_SEQ 507
FT CONFLICT 24
FT CONFLICT 76
FT CONFLICT 160
FT CONFLICT 278
FT CONFLICT 278
FT CONFLICT 390
FT CONFLICT 414
FT CONFLICT 424
FT CONFLICT 431
SQ SEQUENCE 511 AA; 58681 MW; 3935221C9C0C0F0 CRC64;
Query Match 54.0%; Score 241; DB 1; Length 511;
Best Local Similarity 54.2%; Pred. No. 6e-21;
Matches 45; Conservative 14; Mismatches 24; Indels 0; Gaps 0;
QY 1 WLVEGSRREKAEELLPGNPGCAFILRESQTRGSYSLSVRLSRPASWDIRHYRTHCL 60
Db 128 WFFEDITRDADARQLAPGNSACAFILRESSETLGKSGSLSVRDYDPMGCDVYKHYKIRSL 187
QY 61 DNGMLYSPRLFPBLSQALVDHY 83
Db 188 DNGGYISPRITFPCLSDMKHY 210

RESULT 6
LYN_RAT
ID LYN_RAT STRAND: PRT; 511 AA.
AC Q07014; Q63320;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
GN LYN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Minoguchi K., Nishikata H., Stragantian R.P.;
RT "Bacterially expressed rat p56lyn binds several proteins in rat
RT basophilic leukemia cells including pp72, a tyrosine phosphorylated
RT protein prominent in activated cells";
RL J. Immunol. 150:222-222(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94171041; PubMed=8125304;
RA Rider L.G., Raben N., Miller L., Jelsma C.;
RT "The cDNAs encoding two forms of the LYN protein tyrosine kinase are
RT expressed in rat mast cells and human myeloid cells";
RL Gene 138:219-222(1994).
RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97442484; PubMed=9295361;
 RA Vonkhe B.M., Chen H., Haleem-Smith H., Metzger H.;
 RT "The unique domain as the site on Lyn kinase for its constitutive
 association with the high affinity receptor for IgE";
 RL J. Biol. Chem. 272:24072-24080(1997)
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
 CC MYELOID CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL; L14951; AAA41549.1; -;
 DR EMBL; L14782; AAA20944.1; -;
 DR EMBL; L14823; AAA20944.1; -;
 DR EMBL; AF000300; AAB71344.1; -;
 DR EMBL; AF000301; AAB71345.1; -;
 DR EMBL; AF000302; AAB71346.1; -;
 DR HSSP; P08631; 1AD3.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00059; pkinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Wristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0
 FT LIPID 1
 FT LIPID 2
 FT DOMAIN 62 122
 FT DOMAIN 128 225
 FT DOMAIN 246 500
 FT NP BIND 252 260
 FT BINDING 274 274
 FT ACT_SITE 366 366
 FT MOD_RES 396 396
 FT MOD_RES 507 507
 FT VARSPIC 24 44
 FT CONFLICT 230 230
 FT CONFLICT 307 307
 FT CONFLICT 418 418
 SQ SEQUENCE 511 AA; 58529 MW; 24425E229CD43ED CRC64;

Query Match

54.0%; Score 241; DB 1; Length 511;

Best Local Similarity 54.2%; Pred. No. 6e-21;
 Matches 45; Conservative 14; Mismatches 24; Indels 0; Gaps 0;
 QY 1 WLVLGSRKAEKELLPLPGNGAFILRSQTRNGSYSLVRLSPASWDRIRHRIHCL 60
 DB 128 WFFPDIRKRAEQLAFNGSAGAFILRESLTKGSFSLVRYDPMHGDVHKYKIRSL 187
 QY 61 DNGWLYSPLTPPLSQALVDHY 83
 DB 188 DNGGYISPLTPPTCSDMIKY 210
 RESULT 7
 HCK_MOUSE
 ID HCK_MOUSE STANDARD; PRT; 524 AA.
 AC P08103; 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK and P60-HCK)
 DE (Hemopoietic cell kinase) (B-cell/myeloid kinase) (BMK).
 GN HCK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 22-524 FROM N.A.
 RC STRAIN=ICR; TISSUE=Macrophage;
 RX MEDLINE=88067781; PubMed=3684607;
 RA Klemz M.J., McKercher S.R., Maki R.A.;
 RT "Nucleotide sequence of the mouse hck gene";
 RL Nucleic Acids Res. 15:9600-9600(1987).
 RN [2]
 RP SEQUENCE OF 22-524 FROM N.A.
 RX MEDLINE=88068587; PubMed=3317404;
 RA Holtzman D.A., Cook W.D., Dunn A.R.;
 RT "Isolation and sequence of a cDNA corresponding to a src-related gene
 RT expressed in murine hemopoietic cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8325-8329(1987).
 RN [3]
 RP SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
 RX MEDLINE=91342636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization";
 RL Mol. Cell. Biol. 11:4353-4370(1991).
 RL Mol. Cell. Biol. 11:4353-4370(1991).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: P59-HCK AND P56-HCK ARE ASSOCIATED WITH
 CC MEMBRANES. P59-HCK IS ALSO CYTOPLASMIC.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1959-HCK (shown here) and P56-
 CC HCK; are produced by alternative initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 CC MYELOID AND B-LYMPHOID LINEAGES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----

DR EMBL; Y00487; CA68544.1; -
 DR EMBL; J03023; AAA37305.1; -
 DR PIR; A27282; TVMSHC.
 DR PIR; A39973; A39973.
 DR HSSP; P08631; IAD5.
 DR MGD; MGI:96052; HCK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR TRANSFERASE; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain; Alternative initiation.
 FT CHAIN 1 524 TYROSINE-PROTEIN KINASE P59-HCK.
 FT INIT MET 22 524 FOR ISOFORM P56-HCK.
 FT DOMAIN 22 22
 FT DOMAIN 142 229 SH2
 FT DOMAIN 260 513 PROTEIN KINASE
 FT NP BIND 266 274 ATP (BY SIMILARITY).
 FT BINDING 288 288 ATP (BY SIMILARITY).
 FT ACT SITE 379 379 BY SIMILARITY.
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT LIPID 23 23 MYRISTATE (BY SIMILARITY).
 FT MOD RES 409 409 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 524 AA; 59129 MW; DF72PDS9B38C9706 CRC64;

Query Match 53.8%; Score 240; DB 1; Length 524;
 Best Local Similarity 56.6%; Pred. No. 8.1e-21;
 Matches 47; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 1 WLVEGLSRKAEELLPLPQPGAFILRESQTRGSYSVRLSPASWPRIRHYRHL 60
 DB 142 WFKGISKQKDEKHLAPGNMGLSGMINDSTTKGYSLSVDFPDQGHDTGVKIRTL 201
 QY 61 DNGWLISPRITPESLQALVDHY 83
 DB 202 DSGGFYISPRFESLQELVLDHY 224

RESULT 8
 ID BLK_HUMAN STANDARD; PRT; 504 AA.
 AC P51451; Q16291;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase Blk (EC 2.7.1.112) (B lymphocyte kinase) (p55-
 DE BLK).
 GN BLK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCB1_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95123078; PubMed=7822795;

RA Islam K.B., Rabhani H., Larsson C., Sanders R., Smith C.I.;
 RT "Molecular cloning, characterization, and chromosomal localization of
 RT a human lymphoid tyrosine kinase related to murine Blk."
 RT J. Immunol. 154:1265-1272 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95148218; PubMed=7845672;
 RA Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,
 RA Niederhuber J.E.;
 RT "Molecular cloning and chromosomal localization of the human homologue
 RT of a B-lymphocyte specific protein tyrosine kinase (blk)."
 RT Oncogene 10:477-486 (1995).
 CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT
 CC IS RESTRICTED TO B LYMPHOID CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z3398; CA83965.1; -
 DR EMBL; S76617; AAB3365.1; -
 DR HSSP; P16277; IBLK.
 DR Genew; HGNC:1057; BLK.
 DR MIM; 191305; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; FALSE_NEG.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain.
 FT INIT MET 0 0
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 57 117 SH3.
 FT DOMAIN 123 219 SH2.
 FT DOMAIN 240 493 PROTEIN KINASE.
 FT NP BIND 246 254 ATP (BY SIMILARITY).
 FT BINDING 268 268 ATP (BY SIMILARITY).
 FT ACT SITE 359 359 BY SIMILARITY.
 FT MOD RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 286 286 M -> V (IN REF. 2).
 FT CONFLICT 406 406 I -> Y (IN REF. 2).
 SQ SEQUENCE 504 AA; 57607 MW; BD1D505C7370C8 CRC64;

Query Match 52.1%; Score 232.5; DB 1; Length 504;
 Best Local Similarity 54.2%; Pred. No. 6e-20;
 Matches 45; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

OY 1 WLYEGLSPREKARELLLPNGNPGAFIREISOTRSGSYSLVRLSPASMDRIYRIRHIC 60
 DB 123 WFRSOGKEAEAROLAPINKASFLIRSEITNKGRSLSVK-DVTGGLIKHKIKRL 181
 OY 61 DNGMLYISFRLTFPSLQALVDHY 83
 DB 182 DEGYIISPRITFSLQALVQHY 204
 RESULT 9
 LCK_HUMAN
 ID LCK_HUMAN STANDARD; PRT: 508 AA.
 AC P06239; P07100; Q9NTT8; Q96DW4; Q13152; Q12850;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase LCK (BC 2.7.1.112) (P56-LCK)
 DE (LSK) (T cell-specific protein-tyrosine kinase).
 GN LCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OK NCBI_TaxID=9606;
 RN 1
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89123626; PubMed=3265417;
 RA Perlmutter R.M., March J.D., Lewis D.B., Peet R., Ziegler S.F.,
 RA Wilson C.B.;
 RT "Structure and expression of lck transcripts in human lymphoid
 RT cells";
 RL J. Cell. Biochem. 38:117-126(1988).
 RN 12
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87133831; PubMed=3493153;
 RA Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
 RA Mak T.W.;
 RT "A human T cell-specific cDNA clone (Y116) encodes a protein with
 RT extensive homology to a family of protein-tyrosine kinases";
 RL Eur. J. Immunol. 16:1643-1646(1986).
 RN 13
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90108697; PubMed=2558056;
 RA Rouer E., Van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
 RA Benarous R.;
 RT "Structure of the human lck gene: differences in genomic organisation
 RT within src-related genes affect only N-terminal exons";
 RL Gene 84:105-113(1993).
 RN 14
 RP SEQUENCE FROM N.A., VARIANTS L-27, POKP-231 INS; V-352, L-446, AND
 RP PHOSPHORYLATION OF TYR-393 AND TYR-504.
 RC TISSUE=Leukemia;
 RX MEDLINE=9418714; PubMed=819546;
 RA Wright D.D., Sefton B.M., Kamps M.P.;
 RT "Oncogenic activation of the lck protein accompanies translocation of
 RT the lck gene in the human HSB2 T-cell leukemia";
 RL Mol. Cell. Biol. 14:2429-2437(1994).
 RN 15
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Leukemic T-cell;
 RX MEDLINE=96085119; PubMed=7495859;
 RA Vogel L.B., Arthur R., Fujita D.J.;
 RT "An aberrant lck mRNA in two human T-cell lines";
 RL Biochim. Biophys. Acta 1264:168-172(1995).
 RN 16
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph;
 RA Strausberg R.;
 RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 RN 17
 RP SEQUENCE OF 13-508 FROM N.A.
 RC TISSUE=Peripheral blood lymphocytes;
 RX MEDLINE=20462621; PubMed=11009097;
 RA Boncristiano M., Majolini M.B., D'Elia M.M., Pacini S., Valensin S.,
 RA Uivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
 RA Balderi C.T.;
 RT "Defective recruitment and activation of ZAP-70 in common variable
 RT immunodeficiency patients with T cell defects";
 RL Eur. J. Immunol. 30:2632-2638(2000).
 RN 18
 RP SEQUENCE OF 367-508 FROM N.A.
 RX MEDLINE=88217332; PubMed=2835736;
 RA Vallette A., Foss F.M., Sausville E.A., Bojen J.B., Rosen N.;
 RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
 RT and other non-lymphoid human tumor cell lines";
 RL Oncogene Res. 1:357-374(1987).
 RN 19
 RP SEQUENCE OF 374-508 FROM N.A.
 RX MEDLINE=87000726; PubMed=3489486;
 RA Trevillian J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
 RA Lina T.J.;
 RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
 RT p56LCK";
 RL Biochim. Biophys. Acta 888:286-295(1986).
 RN 10
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=8906891; PubMed=2850479;
 RA Garvin A.M., Pawar S., March J.D., Perlmutter R.M.;
 RT "Structure of the murine lck gene and its rearrangement in a murine
 RT lymphoma cell line";
 RL Mol. Cell. Biol. 8:3058-3064(1988).
 RN 11
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=89131764; PubMed=2787474;
 RA Takadera T., Leung S., Gernone A., Koga Y., Takiyama Y.,
 RA Miyamoto N.G., Mak T.W.;
 RT "Structure of the two promoters of the human lck gene: differential
 RT accumulation of two classes of lck transcripts in T cells";
 RL Mol. Cell. Biol. 9:2173-2180(1989).
 RN 12
 RP MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 RT protein expression map database";
 RL Proteomics 2:212-223(2002).
 RN 13
 RP INTERACTION WITH PI3K.
 RX MEDLINE=94067101; PubMed=7504174;
 RA Vogel L.B., Fujita D.J.;
 RT "The SH3 domain of p56lck is involved in binding to
 RT phosphatidylinositol 3'-kinase from T lymphocytes";
 RL Mol. Cell. Biol. 13:7408-7417(1993).
 RN 14
 RP INTERACTION WITH KHDRBS1.
 RX MEDLINE=95153508; PubMed=7852312;
 RA Vogel L.B., Fujita D.J.;
 RT "p70 phosphorylation and binding to p56lck is an early event in
 RT interleukin-2-induced onset of cell cycle progression in
 RT T-lymphocytes";
 RL J. Biol. Chem. 270:2506-2511(1995).
 RN 15
 RP PHOSPHORYLATION OF TYR-504.
 RX MEDLINE=92347326; PubMed=1639064;
 RA Bergman M., Mustelin T., Oecklen C., Partanen J., Flint N.A.,
 RA Amrein K.E., Autero M., Burn P., Allitalo K.;
 RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
 RT down regulates its catalytic activity";
 RL EMBO J. 11:2919-2924(1992).
 RN 16
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 52-225.
 RX MEDLINE=94203291; PubMed=7512222;
 RA Eck M.J., Atweell S.K., Shoelson S.E., Harrison S.C.;

RA Abraham K.M., Levin S.D., March J.D., Forbush K.A., Perlmuter R.M.;
 RT "Thymic tumorigenesis induced by overexpression of p56lck.";
 RN Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
 RP [9]
 RX MUTAGENESIS.
 RA MEDLINE=93133805; PubMed=8421674;
 RT Carrera A.C., Alexandrov K., Roberts T.M.;
 RT "The conserved lysine of the catalytic domain of protein kinases is
 RT actively involved in the phosphotransfer reaction and not required
 RT for anchoring ATP.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
 RN [10]
 RP PALMITOYLATION
 RX MEDLINE=94019312; PubMed=8413237;
 RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
 RT "Palmitoylation of an amino-terminal cysteine motif of protein
 RT tyrosine kinases p56lck and p59fyn mediates interaction with
 RT glycosyl-phosphatidylinositol-anchored proteins.";
 RL Mol. Cell. Biol. 13:6385-6392(1993).
 RN [11]
 RP PALMITOYLATION
 RX MEDLINE=95071286; PubMed=7980442;
 RA Koesgl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.I.;
 RT "Palmitoylation of multiple Src-family kinases at a homologous N-
 RT terminal motif.";
 RL Biochem. J. 303:749-753(1994).
 CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
 CC ITS EARLY EXPRESSION IS ESSENTIAL FOR EARLY T-LYMPHOCTYME
 CC DEVELOPMENT.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
 CC CD4 OR CD8.
 CC -1- TISSUE SPECIFICITY: PRESENT AT A LOW LEVEL IN MOST T CELLS, AND
 CC AT AN ELEVATED LEVEL IN LSTRA AND THY 19 (T-CELL LYMPHOMA) CELLS.
 CC -1- DEVELOPMENTAL STAGE: LEVELS REMAIN RELATIVELY CONSTANT THROUGHOUT
 CC T-CELL ONTOGENY.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X03533; CAA27234.1; -;
 DR EMBL: M12056; AAB59674.1; -;
 DR EMBL: X03533; CAA27235.1; ALT SEQ.
 DR EMBL: X03533; CAA27236.1; ALT SEQ.
 DR EMBL: M21511; AAA39422.1; ALT_SEQ.
 DR EMBL: M18098; AAA39421.1; -;
 DR PIR: A23639; A23639.
 DR HSSP: P06239; 1LCK.
 DR MGD: MGI:96736; LCK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00253; SH2; 1.
 DR SMART: SM00253; SH2; 1.

DR SMART: SM00236; SH3; 1.
 DR SMART: SM00219; TYKIC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;
 KW ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate;
 KW Lipoprotein.
 FT INIT_MET 0 0 PROBABLE.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE.
 FT LIPID 4 4 PALMITATE.
 FT DOMAIN 60 120 SH3.
 FT DOMAIN 126 223 SH2.
 FT DOMAIN 244 497 PROTEIN_KINASE.
 FT NP_BIND 250 258 ATP (BY SIMILARITY).
 FT BINDING 272 272 ATP (BY SIMILARITY).
 FT ACT_SITE 363 363 BY SIMILARITY.
 FT MOD_RES 393 393 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 504 504 PHOSPHORYLATION (NEGATIVE REGULATION) (BY SIMILARITY).
 FT NOTAGEN 268 268 K->N: REDUCED ACTIVITY.
 FT NOTAGEN 269 269 V->L: REDUCED ACTIVITY.
 FT NOTAGEN 270 270 A->S: REDUCED ACTIVITY.
 FT NOTAGEN 271 271 V->A: REDUCED ACTIVITY.
 FT NOTAGEN 272 272 K->R: LOSS OF ACTIVITY.
 FT NOTAGEN 273 272 S->N: REDUCED ACTIVITY.
 FT NOTAGEN 274 274 L->M: REDUCED ACTIVITY.
 FT NOTAGEN 275 275 K->V: REDUCED ACTIVITY.
 FT NOTAGEN 504 504 Y->S: CAUSES THYMIC TUMORS.
 FT CONFLICT 282 283 VP -> DA (IN REF. 2).
 SQ SEQUENCE 508 AA; 57821 MW; B92562498CAF6878 CRC64;
 Query Match 50.9%; Score 227; DB 1; Length 508;
 Best Local Similarity 54.2%; Pred. No. 2, 7e-19;
 Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;
 Qy 1 WYEGLSREKAEKELLPPNPGAFILRESQTRGSYSVLSVLSRPAWDRIRYRINCL 60
 Db 126 WFKXLSRDKAEKQLLPNTGHSFLIRSESTAGSFSLVDFDQNGSVVGHYRNL 185
 Qy 61 DNGWLYISPRITFSPSLQALVDHY 83
 Db 186 DNGGFYISPRITFGHLDVRYH 208
 RESULT 11
 ID BLK_MOUSE STANDARD; PRT; 498 AA.
 AC P16277;
 DT 01-AUG-1990 (Rel. 15. Created)
 DT 01-NOV-1995 (Rel. 32. Last sequence update)
 DT 15-JUN-2002 (Rel. 41. Last annotation update)
 DE Tyrosine-protein kinase BLK (BC 2.7.1.112) (B lymphocyte kinase) (p55-
 DE BLK).
 GN BLK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=90117147; PubMed=2404338;
 RA Dymeck S.M., Niederhuber J.E., Desiderio S.V.;
 RT "Specific expression of a tyrosine kinase gene, blk, in B lymphoid
 RT cells.";
 RL Science 247:332-336(1990).
 RN [2]
 RP STRUCTURE BY NMR OF SH2 DOMAIN.
 RX MEDLINE=96224819; PubMed=8639560;

RA Metzler W.J., Leitling B., Pryor K., Mueller L., Farmer B.T. II.
 RT "The three-dimensional solution structure of the SH2 domain from
 RL p55b1k kinase." Biochemistry 35:6201-6211(1996).
 CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT
 CC IS RESTRICTED TO B LYMPHOID CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M30903; AAA0453.1; -
 DR PIR: A40092; A40092.
 DR PDB: 1BLJ; 12-MAR-97.
 DR PDB: 1BLK; 12-MAR-97.
 DR MGD; MGT:88169; BLK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PRO0401; SH2DOMAIN.
 DR PRINTS: PRO0452; SH3DOMAIN.
 DR PRINTS: PRO0109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN KINASE_TYR; FALSE_NEG.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain; 3D-structure.
 FT INT MET 0
 FT LIPID 1
 FT DOMAIN 1 111 MYRISTATE (BY SIMILARITY).
 FT 117 213 SH3.
 FT DOMAIN 117 213 SH3.
 FT 234 487 PROTEIN KINASE.
 FT NP BIND 240 248 ATP (BY SIMILARITY).
 FT BINDING 262 262 ATP (BY SIMILARITY).
 FT ACT SITE 353 353 BY SIMILARITY.
 FT MOD RES 382 382 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 498 AA; 56513 MW; BE49DB079FDD577 CRG4;
 Query Match 50.3%; Score 224.5; DB 1; Length 498;
 Best Local Similarity 51.8%; Pred. No. 5,3e-19;
 Matches 43; Conservative 16; Mismatches 23; Indels 1; Gaps 1;

RESULT 12
 LCK CHICK
 ID LCK CHICK STANDARD; PRT; 507 AA.
 AC P42683;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-
 DE tyrosine kinase C-TKL).
 GN LCK.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxId=9031;
 RN [1]
 RP SEQUENCE OF 1-89 FROM N.A.
 RX MEDLINE=92186854; PubMed=1545804;
 RA Chow L., Ratcliffe M., Veillette A.;
 RT "tkl is the avian homolog of the mammalian lck tyrosine protein
 RT kinase gene." Mol. Cell. Biol. 12:1226-1233(1992).
 RL [2]
 RN SEQUENCE OF 46-507 FROM N.A.
 RX MEDLINE=88097370; PubMed=3321053;
 RA Streibhardt K., Mullins J.T., Bruck C., Ruebsamen-Waigmann H.;
 RT "Additional member of the protein-tyrosine kinase family: the src-
 RT and lck-related protooncogene c-tkl." Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).
 RL [3]
 CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
 CC CD4 OR CD8.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
 DR EMBL: M85043; AAA4903.1; -
 DR EMBL: J03579; AAA4981.1; ALT_INIT.
 DR HSP; P06239; 3LCK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PRO0401; SH2DOMAIN.
 DR PRINTS: PRO0452; SH3DOMAIN.
 DR PRINTS: PRO0109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;
 KW ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate;

KM Lipoprotein. 0 0 PROBABLE. (BY SIMILARITY).
 FT INIT MET 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT LIPID 4 4 PALMITATE (BY SIMILARITY).
 FT DOMAIN 59 119 SH3.
 FT DOMAIN 125 222 SH2.
 FT DOMAIN 243 496 PROTEIN KINASE.
 FT NP BIND 249 257 ATP (BY SIMILARITY).
 FT BINDING 271 271 ATP (BY SIMILARITY).
 FT ACT SITE 362 362 BY SIMILARITY.
 FT MOD RES 392 392 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 503 503 PHOSPHORYLATION (NEGATIVE REGULATION) (BY SIMILARITY).
 SQ SEQUENCE 507 AA; 5808 MW; EC83C4FA891B6170 CRC64;
 Query Match 50.0%; Score 223; DB 1; Length 507;
 Best Local Similarity 53.0%; Pred. No. 8.2e-19;
 Matches 44; Conservative 14; Mismatches 25; Indels 0; Gaps 0;
 QY 1 MWELGSRKAEKELLPGPGAFIRESGTGRGYSVLSRPAAMDRIHYRIHCL 60
 DB 125 WFKNSLRKNAEARLNLASGNTGSHFLIRESETSKGYSLSVDPDQNGETVYKIRNM 184
 QY 61 DNGWLYISPRLTSPSLQALVDHY 83
 DB 185 DNGGYISPRVTFSLHELVY 207
 RESULT 13
 YES_XIPHE STANDARD; PRT; 544 AA.
 ID YES_XIPHE
 AC P27447;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (P61-YES) (C-YES).
 GN YES.
 OS Xiphophorus helleri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 NC NCBI_TaxID=8084;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rio Lancetilla;
 RX MEDLINE=91187435; PubMed=1707152;
 RA Hennig G., Ottillie S., Scharf M.;
 RT "Conservation of structure and expression of the c-yes and fyn genes in lower vertebrates.";
 RL Oncogene 6:361-369(1991).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUPFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 CC EMBL; X54970; CAA38714.1; -.
 CC HSSP; P12931; IFWK.
 CC InterPro; IPR000719; Euk_pkinase.
 CC InterPro; IPR000980; SH2.
 CC InterPro; IPR01452; SH3.

DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; PFO0017; SH2; 1.
 DR Pfam; PFO0018; SH3; 1.
 DR Pfam; PFO0069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH2; 1.
 DR ProDom; PD000093; SH3; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KM Transferase; ATP-binding; Myristate; SH3 domain; SH2 domain.
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT DOMAIN 92 153 SH3.
 FT DOMAIN 159 256 SH2.
 FT DOMAIN 278 531 PROTEIN KINASE.
 FT NP BIND 284 292 ATP (BY SIMILARITY).
 FT BINDING 306 306 ATP (BY SIMILARITY).
 FT ACT SITE 397 397 BY SIMILARITY.
 FT MOD_RES 427 427 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 544 AA; 61288 MW; 7D41818B3E7086EF CRC64;
 Query Match 48.7%; Score 217; DB 1; Length 544;
 Best Local Similarity 54.2%; Pred. No. 4.6e-18;
 Matches 45; Conservative 9; Mismatches 29; Indels 0; Gaps 0;
 QY 1 MWELGSRKAEKELLPGPGAFIRESGTGRGYSVLSRPAAMDRIHYRIHCL 60
 DB 159 WYFGLSRKOTERLLLPNGRGFFLIRESETTKGAYSLRDWDETGDCKGHYKIRKL 218
 QY 61 DNGWLYISPRLTSPSLQALVDHY 83
 DB 219 DNGGYITRTQPSLQALVDHY 241
 RESULT 14
 YES_XENLA STANDARD; PRT; 537 AA.
 ID YES_XENLA
 AC P10536;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (P61-YES) (C-YES).
 GN YES.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89296347; PubMed=2472592;
 RX Steele R.E., Irwin M.Y., Knudsen C.L., Collett J.W., Fero J.B.;
 RT "The yes proto-oncogene is present in amphibians and contributes to the maternal RNA pool in the oocyte.";
 RL Oncogene Res. 4:223-233(1989).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUPFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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CC -----
DR EMBL; X14377; CAA32551.1; -.
DR PIR; S08517; S08517.
DR HSSP; P00523; 2PTRK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KM Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
KW Transferase; ATP-binding; Myristate; SH3 domain; SH2 domain.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT DOMAIN 85 146 SH3.
FT DOMAIN 152 249 SH2.
FT NP BIND 271 524 PROTEIN_KINASE.
FT BINDING 277 285 ATP (BY SIMILARITY).
FT ACT SITE 299 299 ATP (BY SIMILARITY).
FT MOD RES 420 420 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 537 AA; 60357 MW; FFE2F615940AC31B CRC64;

Query Match 48.2%; Score 215; DB 1; Length 537;
Best Local Similarity 50.0%; Pred. No. 7.8e-18;
Matches 44; Conservative 11; Mismatches 23; Indels 10; Gaps 2;

QY 1 WLVEGLSREKAEELLLPNCQAFLLRESQTRGSGSYLSVRLSPASWDRIR-----HY 55
DB 153 WYFGKMKRKAERLLNPNQNGRTFLVRESEETTKAYISLSIR-----DMDVKGDNVKEY 206
QY 56 RHCLDNGMLYISPRITPSPQLADVHY 83
DB 207 KIRKLDNGGYITTTAQPESLQKLVKEY 234

RESULT 15
YES CHICK STANDARD; PRT; 541 AA.
AC P09324;
DT 01-MAR-1989 (Rel. 10; Created)
DT 01-MAR-1989 (Rel. 10; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (p61-YES)
DE (C-YES).
GN YES.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=89041591; PubMed=3054816;
RA Sudol M., Kiehwetter C., Zhao Y.H., Dorai T., Wang L.H.,
RA Hanafusa H.;
RT "Nucleotide sequence of a cDNA for the chick yes proto-oncogene:
RT comparison with the viral yes gene.";
RL Nucleic Acids Res. 16:9876-9876 (1988).
RN [2]
RP REVISION TO 232.
RA Sudol M.;
RL Submitted (NOV-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Brain;
RX MEDLINE=89128204; PubMed=2464785;
RA Zheng X., Podell S., Sefton B.M., Kaplan P.L.;
RT "The sequence of chicken c-yes and p61c-yes.";
RT Oncogene 4:99-104 (1989).
RN [4]
RP SEQUENCE OF 396-451 FROM N.A.
RX MEDLINE=93096482; PubMed=1281306;
RA Marcelle C., Bichmann A.;
RT "Molecular cloning of a family of protein kinase genes expressed in
RT the avian embryo.";
RT Oncogene 7:2479-2487 (1992).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
DR EMBL; X13207; CAA31595.1; -.
DR EMBL; X12461; CAA31002.1; -.
DR EMBL; X69695; CAA49365.1; -.
DR PIR; S0324; TVCHVS.
DR HSSP; P00523; 2PTRK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KM Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
KW Transferase; ATP-binding; Myristate; SH3 domain; SH2 domain.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT DOMAIN 89 150 SH3.
FT DOMAIN 156 253 SH2.
FT NP BIND 275 528 PROTEIN_KINASE.
FT BINDING 281 289 ATP (BY SIMILARITY).
FT ACT SITE 303 303 ATP (BY SIMILARITY).

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